

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/069,541  
Source: JFW16  
Date Processed by STIC: 10/25/2005

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 10/25/2005

PATENT APPLICATION: US/10/069,541

TIME: 08:11:53

Input Set : A:\HAGA SEQUENCE LISTING.txt

Output Set: N:\CRF4\10252005\J069541.raw

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3 <110> APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
5 <120> TITLE OF INVENTION: High-Affinity Choline Transporter
7 <130> FILE REFERENCE: A011-05PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/069,541
C--> 10 <141> CURRENT FILING DATE: 2002-02-27
12 <150> PRIOR APPLICATION NUMBER: JP 11/240642
13 <151> PRIOR FILING DATE: 1999-08-27
15 <150> PRIOR APPLICATION NUMBER: JP 11/368991
16 <151> PRIOR FILING DATE: 1999-12-27
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1731
24 <212> TYPE: DNA
25 <213> ORGANISM: Caenorhabditis elegans
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1731)
31 <400> SEQUENCE: 1
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33 Met Ala Asp Leu Leu Gly Ile Val Ala Ile Val Phe Phe Tyr Val Leu
34 1 5 10 15
36 att ctt gtc gtt gga ata tgg gcg ggt aga aaa tcg aaa agt tca aaa 96
37 Ile Leu Val Val Gly Ile Trp Ala Gly Arg Lys Ser Lys Ser Ser Lys
38 20 25 30
40 gag ctt gaa tca gaa gcc gcc gcg gcg acg gaa gag gtg atg tta gct 144
41 Glu Leu Glu Ser Glu Ala Gly Ala Ala Thr Glu Glu Val Met Leu Ala
42 35 40 45
44 ggg aga aac atc gga act ctt gtc gga att ttc aca atg act gcc acg 192
45 Gly Arg Asn Ile Gly Thr Leu Val Gly Ile Phe Thr Met Thr Ala Thr
46 50 55 60
48 tgg gtt ggc ggt gct tat atc aat gga acc gcc gag gct ctg tat aat 240
49 Trp Val Gly Gly Ala Tyr Ile Asn Gly Thr Ala Glu Ala Leu Tyr Asn
50 65 70 75 80
52 gga ggt ctc ctt gga tgt cag gct cca gtt gga tat gca att tcc ctt 288
53 Gly Gly Leu Leu Gly Cys Gln Ala Pro Val Gly Tyr Ala Ile Ser Leu
54 85 90 95
56 gtt atg gga gga cta ctt ttc gca aag aaa atg cga gaa gaa gga tat 336
57 Val Met Gly Gly Leu Leu Phe Ala Lys Lys Met Arg Glu Glu Gly Tyr
58 100 105 110
60 att aca atg ctc gat cct ttt cag cac aaa tat ggc caa cga atc ggt 384
61 Ile Thr Met Leu Asp Pro Phe Gln His Lys Tyr Gly Gln Arg Ile Gly
62 115 120 125

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64 ggc ttg atg tat gtt cca gca ctt ctt ggt gaa aca ttc tgg aca gca 432
65 Gly Leu Met Tyr Val Pro Ala Leu Leu Gly Glu Thr Phe Trp Thr Ala
66      130      135      140
68 gcc att ctt tcg gca ctt ggt gca aca ctg tcg gta att ctt gga atc 480
69 Ala Ile Leu Ser Ala Leu Gly Ala Thr Leu Ser Val Ile Leu Gly Ile
70 145      150      155      160
72 gac atg aat gca tca gtg acc ctg tcg gcc tgt att gcc gta ttc tac 528
73 Asp Met Asn Ala Ser Val Thr Leu Ser Ala Cys Ile Ala Val Phe Tyr
74      165      170      175
76 aca ttc acc ggt gga tac tat gca gtc gcg tac act gac gtc gtt caa 576
77 Thr Phe Thr Gly Gly Tyr Tyr Ala Val Ala Tyr Thr Asp Val Val Gln
78      180      185      190
80 cta ttt tgc att ttc gtc ggt ttg tgg gtt tgc gtg ccg gcg gct atg 624
81 Leu Phe Cys Ile Phe Val Gly Leu Trp Val Cys Val Pro Ala Ala Met
82      195      200      205
84 gtg cat gat ggt gcg aag gat att tcc agg aat gca ggc gac tgg att 672
85 Val His Asp Gly Ala Lys Asp Ile Ser Arg Asn Ala Gly Asp Trp Ile
86      210      215      220
88 gga gag att gga gga ttc aaa gaa aca tct ctc tgg att gat tgc atg 720
89 Gly Glu Ile Gly Gly Phe Lys Glu Thr Ser Leu Trp Ile Asp Cys Met
90 225      230      235      240
92 ctt ctc ctt gtc ttt gga gga att cca tgg caa gtg tac ttc caa aga 768
93 Leu Leu Leu Val Phe Gly Gly Ile Pro Trp Gln Val Tyr Phe Gln Arg
94      245      250      255
96 gtt ctc tcc tca aaa act gct cat gga gca cag acg ttg tcg ttt gtg 816
97 Val Leu Ser Ser Lys Thr Ala His Gly Ala Gln Thr Leu Ser Phe Val
98      260      265      270
100 gcg ggc gtc gga tgc att ctc atg gcg att cca cca gcg ttg atc ggt 864
101 Ala Gly Val Gly Cys Ile Leu Met Ala Ile Pro Pro Ala Leu Ile Gly
102      275      280      285
104 gca att gcc agg aac aca gac tgg aga atg act gat tat tcc cca tgg 912
105 Ala Ile Ala Arg Asn Thr Asp Trp Arg Met Thr Asp Tyr Ser Pro Trp
106      290      295      300
108 aac aat gga act aag gtc gaa tcg att cca ccg gat aag aga aac atg 960
109 Asn Asn Gly Thr Lys Val Glu Ser Ile Pro Pro Asp Lys Arg Asn Met
110 305      310      315      320
112 gtg gtc ccg ttg gta ttc cag tat ctt acg cca aga tgg gtc gcc ttt 1008
113 Val Val Pro Leu Val Phe Gln Tyr Leu Thr Pro Arg Trp Val Ala Phe
114      325      330      335
116 att gga ctc ggc gca gtg tcg gct gct gta atg tca tct gca gat tca 1056
117 Ile Gly Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser
118      340      345      350
120 tct gta cta tca gca gca tca atg ttt gct cac aac atc tgg aag ctc 1104
121 Ser Val Leu Ser Ala Ala Ser Met Phe Ala His Asn Ile Trp Lys Leu
122      355      360      365
124 aca att cgc cct cac gcg tct gaa aaa gaa gtg ata att gtg atg aga 1152
125 Thr Ile Arg Pro His Ala Ser Glu Lys Glu Val Ile Ile Val Met Arg
126      370      375      380
128 ata gcc atc atc tgt gtt ggt atc atg gca acc atc atg gca ctt acc 1200

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129 Ile Ala Ile Ile Cys Val Gly Ile Met Ala Thr Ile Met Ala Leu Thr
130 385                      390                      395                      400
132 att caa tcc atc tat ggg ctt tgg tat ctt tgt gca gat ttg gtc tac 1248
133 Ile Gln Ser Ile Tyr Gly Leu Trp Tyr Leu Cys Ala Asp Leu Val Tyr
134                      405                      410                      415
136 gtc ata ctc ttc cct caa cta tta tgt gtt gta tat atg cca cgt agc 1296
137 Val Ile Leu Phe Pro Gln Leu Leu Cys Val Val Tyr Met Pro Arg Ser
138                      420                      425                      430
140 aat acg tat ggc tca ttg gct ggc tat gca gtc ggt ctt gtg ctc cgt 1344
141 Asn Thr Tyr Gly Ser Leu Ala Gly Tyr Ala Val Gly Leu Val Leu Arg
142                      435                      440                      445
144 ttg att gga ggc gag cca ctt gta tcg ctg cca gcg ttc ttc cat tat 1392
145 Leu Ile Gly Gly Glu Pro Leu Val Ser Leu Pro Ala Phe Phe His Tyr
146                      450                      455                      460
148 cca atg tat acg gat ggg gta cag tat ttc cca ttc agg aca act gct 1440
149 Pro Met Tyr Thr Asp Gly Val Gln Tyr Phe Pro Phe Arg Thr Thr Ala
150 465                      470                      475                      480
152 atg tta tct tca atg gct act atc tac att gta tca ata caa tcg gag 1488
153 Met Leu Ser Ser Met Ala Thr Ile Tyr Ile Val Ser Ile Gln Ser Glu
154                      485                      490                      495
156 aag ctg ttc aaa tcg gga cgt ttg tct ccg gag tgg gac gta atg ggt 1536
157 Lys Leu Phe Lys Ser Gly Arg Leu Ser Pro Glu Trp Asp Val Met Gly
158                      500                      505                      510
160 tgt gta gtg aat att ccg ata gat cat gta ccc ctt ccg tca gat gta 1584
161 Cys Val Val Asn Ile Pro Ile Asp His Val Pro Leu Pro Ser Asp Val
162                      515                      520                      525
164 tcg ttt gct gtt agt agt gag acc ttg aat atg aag gct cca aac gga 1632
165 Ser Phe Ala Val Ser Ser Glu Thr Leu Asn Met Lys Ala Pro Asn Gly
166                      530                      535                      540
168 aca ccg gct cca gta cat ccg aac caa cag ccg tct gat gaa aat aca 1680
169 Thr Pro Ala Pro Val His Pro Asn Gln Gln Pro Ser Asp Glu Asn Thr
170 545                      550                      555                      560
172 tta tta cat cca tat tcg gac caa agt tat tat tcc aca aat agc aat 1728
173 Leu Leu His Pro Tyr Ser Asp Gln Ser Tyr Tyr Ser Thr Asn Ser Asn
174                      565                      570                      575
176 taa 1731
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 576
182 <212> TYPE: PRT
183 <213> ORGANISM: Caenorhabditis elegans
185 <400> SEQUENCE: 2
186 Met Ala Asp Leu Leu Gly Ile Val Ala Ile Val Phe Phe Tyr Val Leu
187 1 5 10 15
188 Ile Leu Val Val Gly Ile Trp Ala Gly Arg Lys Ser Lys Ser Ser Lys
189 20 25 30
190 Glu Leu Glu Ser Glu Ala Gly Ala Thr Glu Glu Val Met Leu Ala
191 35 40 45
192 Gly Arg Asn Ile Gly Thr Leu Val Gly Ile Phe Thr Met Thr Ala Thr
193 50 55 60

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194 Trp Val Gly Gly Ala Tyr Ile Asn Gly Thr Ala Glu Ala Leu Tyr Asn
195 65 70 75 80
196 Gly Gly Leu Leu Gly Cys Gln Ala Pro Val Gly Tyr Ala Ile Ser Leu
197 85 90 95
198 Val Met Gly Gly Leu Leu Phe Ala Lys Lys Met Arg Glu Glu Gly Tyr
199 100 105 110
200 Ile Thr Met Leu Asp Pro Phe Gln His Lys Tyr Gly Gln Arg Ile Gly
201 115 120 125
202 Gly Leu Met Tyr Val Pro Ala Leu Leu Gly Glu Thr Phe Trp Thr Ala
203 130 135 140
204 Ala Ile Leu Ser Ala Leu Gly Ala Thr Leu Ser Val Ile Leu Gly Ile
205 145 150 155 160
206 Asp Met Asn Ala Ser Val Thr Leu Ser Ala Cys Ile Ala Val Phe Tyr
207 165 170 175
208 Thr Phe Thr Gly Tyr Tyr Ala Val Ala Tyr Thr Asp Val Val Gln
209 180 185 190
210 Leu Phe Cys Ile Phe Val Gly Leu Trp Val Cys Val Pro Ala Ala Met
211 195 200 205
212 Val His Asp Gly Ala Lys Asp Ile Ser Arg Asn Ala Gly Asp Trp Ile
213 210 215 220
214 Gly Glu Ile Gly Gly Phe Lys Glu Thr Ser Leu Trp Ile Asp Cys Met
215 225 230 235 240
216 Leu Leu Leu Val Phe Gly Gly Ile Pro Trp Gln Val Tyr Phe Gln Arg
217 245 250 255
218 Val Leu Ser Ser Lys Thr Ala His Gly Ala Gln Thr Leu Ser Phe Val
219 260 265 270
220 Ala Gly Val Gly Cys Ile Leu Met Ala Ile Pro Pro Ala Leu Ile Gly
221 275 280 285
222 Ala Ile Ala Arg Asn Thr Asp Trp Arg Met Thr Asp Tyr Ser Pro Trp
223 290 295 300
224 Asn Asn Gly Thr Lys Val Glu Ser Ile Pro Pro Asp Lys Arg Asn Met
225 305 310 315 320
226 Val Val Pro Leu Val Phe Gln Tyr Leu Thr Pro Arg Trp Val Ala Phe
227 325 330 335
228 Ile Gly Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser
229 340 345 350
230 Ser Val Leu Ser Ala Ala Ser Met Phe Ala His Asn Ile Trp Lys Leu
231 355 360 365
232 Thr Ile Arg Pro His Ala Ser Glu Lys Glu Val Ile Ile Val Met Arg
233 370 375 380
234 Ile Ala Ile Ile Cys Val Gly Ile Met Ala Thr Ile Met Ala Leu Thr
235 385 390 395 400
236 Ile Gln Ser Ile Tyr Gly Leu Trp Tyr Leu Cys Ala Asp Leu Val Tyr
237 405 410 415
238 Val Ile Leu Phe Pro Gln Leu Leu Cys Val Val Tyr Met Pro Arg Ser
239 420 425 430
240 Asn Thr Tyr Gly Ser Leu Ala Gly Tyr Ala Val Gly Leu Val Leu Arg
241 435 440 445
242 Leu Ile Gly Gly Glu Pro Leu Val Ser Leu Pro Ala Phe Phe His Tyr

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243      450      455      460
244 Pro Met Tyr Thr Asp Gly Val Gln Tyr Phe Pro Phe Arg Thr Thr Ala
245 465      470      475      480
246 Met Leu Ser Ser Met Ala Thr Ile Tyr Ile Val Ser Ile Gln Ser Glu
247      485      490      495
248 Lys Leu Phe Lys Ser Gly Arg Leu Ser Pro Glu Trp Asp Val Met Gly
249      500      505      510
250 Cys Val Val Asn Ile Pro Ile Asp His Val Pro Leu Pro Ser Asp Val
251      515      520      525
252 Ser Phe Ala Val Ser Ser Glu Thr Leu Asn Met Lys Ala Pro Asn Gly
253      530      535      540
254 Thr Pro Ala Pro Val His Pro Asn Gln Gln Pro Ser Asp Glu Asn Thr
255 545      550      555      560
256 Leu Leu His Pro Tyr Ser Asp Gln Ser Tyr Tyr Ser Thr Asn Ser Asn
257      565      570      575
261 <210> SEQ ID NO: 3
262 <211> LENGTH: 1743
263 <212> TYPE: DNA
264 <213> ORGANISM: Rattus norvegicus
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(1743)
270 <400> SEQUENCE: 3
271 atg cct ttc cat gta gaa gga cta gta gcg att atc ctg ttc tac ctt 48
272 Met Pro Phe His Val Glu Gly Leu Val Ala Ile Ile Leu Phe Tyr Leu
273 1 5 10 15
275 ctt ata ttt ctg gtt gga ata tgg gct gca tgg aaa acc aaa aac agc 96
276 Leu Ile Phe Leu Val Gly Ile Trp Ala Ala Trp Lys Thr Lys Asn Ser
277 20 25 30
279 ggt aat gca gaa gaa cgc agc gaa gcc atc ata gtt ggg ggc cga gac 144
280 Gly Asn Ala Glu Glu Arg Ser Glu Ala Ile Ile Val Gly Gly Arg Asp
281 35 40 45
283 att ggt ttg ttg gtt ggt ggt ttt acc atg aca gcc acc tgg gtt gga 192
284 Ile Gly Leu Leu Val Gly Gly Phe Thr Met Thr Ala Thr Trp Val Gly
285 50 55 60
287 gga ggt tac atc aac ggg aca gct gaa gca gtt tat ggg cca ggt tgt 240
288 Gly Gly Tyr Ile Asn Gly Thr Ala Glu Ala Val Tyr Gly Pro Gly Cys
289 65 70 75 80
291 ggt cta gct tgg gct cag gca ccc att gga tat tct ctg agt ctg att 288
292 Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile
293 85 90 95
295 tta ggt ggc ctg ttt ttt gca aaa cct atg cgt tcc aag gga tat gtg 336
296 Leu Gly Gly Leu Phe Phe Ala Lys Pro Met Arg Ser Lys Gly Tyr Val
297 100 105 110
299 act atg tta gac ccg ttt caa cag atc tat gga aag cgc atg ggt ggg 384
300 Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly
301 115 120 125
303 ctg ctg ttc atc cct gca ctg atg gga gag atg ttc tgg gct gca gca 432
304 Leu Leu Phe Ile Pro Ala Leu Met Gly Glu Met Phe Trp Ala Ala Ala

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**VERIFICATION SUMMARY**

DATE: 10/25/2005

PATENT APPLICATION: US/10/069,541

TIME: 08:11:54

Input Set : A:\HAGA SEQUENCE LISTING.txt

Output Set: N:\CRF4\10252005\J069541.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date